

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:39:12 ; Search time 26.6 Seconds
(without alignments)
910.658 Million cell updates/sec

Title: US-09-483-543A-8
Perfect score: 1693
Sequence: 1 KRGGAGNFDSEERSWYGR.....QONPDEDFSCGXGLEVLQF 318
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 C_{rk}

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1612	95.2	304	2 I58394	C-Crk - mouse
2	1588	93.8	304	2 A45022	CRK-II - human
3	1379.5	81.5	305	1 A49011	C-Crk - chicken
4	1078	63.7	239	2 A46243	epidermal growth f
5	1052	62.1	204	2 B45022	CRK-I - human
6	917.5	54.2	303	2 S41754	CRKL protein - hum
7	911.5	53.8	303	2 S58352	SH2/SH3 adaptor pr
8	834.5	49.3	259	2 A44988	transforming prote
9	818.5	48.3	232	1 TVFV10	transforming prote
10	236	13.9	211	2 A46444	SH2-SH3 adaptor pr
11	224	13.2	217	2 S26050	growth factor rece
12	224	13.2	217	2 A54688	modular adaptor Gr
13	224	13.2	217	2 A33321	growth factor rece
14	218	12.9	217	2 JT0664	growth factor rece
15	202	11.9	228	2 S25730	SH2-SH3 protein se
16	184	10.9	1291	2 S00666	1-phosphatidylinos
17	182	10.8	1097	2 T31504	hypothetical prote
18	178	10.5	1290	2 A36466	1-phosphatidylinos
19	177	10.5	1290	2 A31317	1-phosphatidylinos
20	172.5	10.2	839	1 TVHUVV	transforming prote
21	170	10.0	816	2 T17257	hypothetical prote
22	167	9.9	844	1 TVMSVV	transforming prote
23	165	9.7	1270	2 T09194	adaptor protein in
24	164	9.7	1196	2 T14108	SH3-containing pro
25	161	9.5	1094	2 T13053	dynamlin associated
26	158.5	9.4	330	2 JE0376	Grb-2 related adap
27	154.5	9.1	878	2 I51940	gene VAV2 protein
28	152.5	9.0	1011	2 T13055	dynamlin associated
29	151.5	8.9	334	2 T33836	hypothetical prote

30	151	8.9	1168	1 MWAXIC	myosin heavy chain
31	150	8.9	960	1 A39651	discs-large tumor
32	149	8.8	639	2 T13151	adaptor protein CM
33	148.5	8.8	1113	1 A47106	myosin heavy chain
34	148	8.7	290	2 T42526	hypothetical prote
35	148	8.7	443	2 T27877	hypothetical prote
36	147	8.7	1044	2 S01966	GTPase-activating
37	146.5	8.7	1038	2 JT0663	ras GTPase-activat
38	146	8.6	946	2 I38100	rho-GTPase-activat
39	144.5	8.5	1047	2 A40121	GTPase-activating
40	143.5	8.5	870	2 B40121	GTPase-activating
41	142	8.4	450	2 A41973	protein-tyrosine k
42	141	8.3	665	2 JC7191	85K c-Cbl-interact
43	139.5	8.2	1236	1 A53970	1-phosphatidylinos
44	139	8.2	359	2 S27788	neutrophil oxidase
45	139	8.2	557	2 A00629	protein-tyrosine k

ALIGNMENTS

RESULT 1
I58394
C-Crk - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I58394
R:Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.; Hiran
Oncogene 9, 1669-1678, 1994
A:Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates ty
A:Reference number: I58394; MUID:94239744
A:Accession: I58394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-304 <RES>
A:Cross-References: GB:S72408; NID:g632866; PIDN:AAB30755.1; PID:g632867
C:Genetics:
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:13-118/Domain: SH2 homology <SH2>
F:139-187/Domain: SH3 homology <SH3>

Query Match	95.2%	Score	1612;	DB 2;	Length	304;			
Best Local Similarity	100.0%;	Pred. No.	3.1e-113;						
Matches	303;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	5	AGNFDSEERSWYGRLSRQEAVALLOGRHGVFLVRDSS	TSPGDYVLSVSENSRVSHYI	64					
Db	2	AGNFDSEERSWYGRLSRQEAVALLOGRHGVFLVRDSS	TSPGDYVLSVSENSRVSHYI	61					
QY	65	INSSGPRPPVPPSPAQPPGVSPSRLRIGDQDFDSL	PALLEFYKHYLDTTTLTEPVARS	124					
Db	62	INSSGPRPPVPPSPAQPPGVSPSRLRIGDQDFDSL	PALLEFYKHYLDTTTLTEPVARS	121					
QY	125	ROGSGVILRQEEAYVRALFDNFNGDEEDLPFKGDI	LIRDKPQEWNAEDSEGKRG	184					
Db	122	ROGSGVILRQEEAYVRALFDNFNGDEEDLPFKGDI	LIRDKPQEWNAEDSEGKRG	181					
QY	185	IPVPVVKYRPASASVSA	LGNGEGSHPPQLGGPEGPYAPQSVNTPPLNQNGPIYAR	244					
Db	182	IPVPVVKYRPASASVSA	LGNGEGSHPPQLGGPEGPYAPQSVNTPPLNQNGPIYAR	241					
QY	245	VIQKRPVNPAYDKTALA	LEVGLVKVTKINVSGWEGECNGKRGHPFFTHVRLDQQNPDE	304					
Db	242	VIQKRPVNPAYDKTALA	LEVGLVKVTKINVSGWEGECNGKRGHPFFTHVRLDQQNPDE	301					
QY	305	DFS	307						
Db	302	DFS	304						
RESULT	2								

A45022 CRK-II - human
C:Species: Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Jun-2000
C:Accession: A45022
R: Matsuda, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A: Title: Two species of human CRK cDNA encode proteins with distinct biological activities
A: Reference number: A45022; MUID: 92334347
A: Accession: A45022
A: Status: Preliminary
A: Molecule type: mRNA
A: Residues: 1-304 <MAT>
A: Cross-references: GB:D10656; NID: g219554; PIDN: BAA01505.1; PID: g219555
A: Experimental source: Placenta
A: Note: sequence extracted from NCBI backbone (NCBIN:108769, NCBIPI:108770)
C: Superfamily: crk transforming protein; SH2 homology; SH3 homology
F: 13-118/Domain: SH2 homology #status atypical <SH2>
F: 139-187/Domain: SH3 homology <SH3>

Query Match 93.8%; Score 1588; DB 2; Length 304;
Best Local Similarity 98.7%; Pred. No. 1.9e-111;
Matches 299; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64
DB 2 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 61

QY 65 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALLEFYKHYLDTTTLIEPVARS 124
DB 62 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALLEFYKHYLDTTTLIEPVARS 121

QY 125 RQSGVILRQEAAYRVALFDNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 184
DB 122 RQSGVILRQEAAYRVALFDNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 181

QY 185 IPVYVEKYRPPASVSALIGNQSGHPQLGGPEPGPYAQPVSNTPLPLNONGPIYAR 244
DB 182 IPVYVEKYRPPASVSALIGNQSGHPQLGGPEPGPYAQPVSNTPLPLNONGPIYAR 241

QY 245 VTQKRVNPAYDKTALALEVGLVKVTKINVSGQWEGECNGKRGHPFTHVRLDQONPD 304
DB 242 VTQKRVNPAYDKTALALEVGLVKVTKINVSGQWEGECNGKRGHPFTHVRLDQONPD 301

QY 305 DFS 307
DB 302 DFS 304

RESULT 3
A49011 c-Crk - chicken
C: Species: Gallus gallus (chicken)
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C: Accession: A49011
R: Reichman, C.T.; Mayer, B.J.; Keshav, S.; Hanafusa, H.
Cell Growth Differ. 3, 451-460, 1992
A: Title: The product of the cellular crk gene consists primarily of SH2 and SH3 regions.
A: Reference number: A49011; MUID: 93041379
A: Accession: A49011
A: Status: Preliminary
A: Molecule type: mRNA
A: Residues: 1-305 <REI>
A: Cross-references: GB:L08168; GB:M32398; NID: g212527; PIDN: AAA49001.1; PID: g212528
A: Experimental source: embryo, brain
A: Note: sequence extracted from NCBI backbone (NCBIN:117106, NCBIPI:117107)
C: Superfamily: crk transforming protein; SH2 homology; SH3 homology
F: 13-119/Domain: SH2 homology <SH2>
F: 140-188/Domain: SH3 homology <SH3>

Query Match 81.5%; Score 1379.5; DB 1; Length 305;

Best Local Similarity 84.5%; Pred. No. 7.2e-96;
Matches 257; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

QY 5 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64
DB 2 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 61

QY 65 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALLEFYKHYLDTTTLIEPVARS 123
DB 62 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALLEFYKHYLDTTTLIEPVARS 121

QY 124 RQSGVILRQEAAYRVALFDNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 183
DB 122 RQSGVILRQEAAYRVALFDNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 181

QY 184 IPVYVEKYRPPASVSALIGNQSGHPQLGGPEPGPYAQPVSNTPLPLNONGPIYAR 243
DB 182 IPVYVEKYRPPASVSALIGNQSGHPQLGGPEPGPYAQPVSNTPLPLNONGPIYAR 241

QY 244 VTQKRVNPAYDKTALALEVGLVKVTKINVSGQWEGECNGKRGHPFTHVRLDQONPD 303
DB 242 VTQKRVNPAYDKTALALEVGLVKVTKINVSGQWEGECNGKRGHPFTHVRLDQONPD 301

QY 304 DFS 307
DB 302 DFS 305

RESULT 4
A46243 epidermal growth factor-receptor-binding protein GRB-3 - mouse (fragment)
C: Species: Mus musculus (house mouse)
C: Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C: Accession: A46243
R: Hargolis, B.; Silvennoinen, O.; Comoglio, F.; Roonprapant, C.; Skolnik, E.; Ullrich
Proc. Natl. Acad. Sci. U.S.A. 89, 8894-8898, 1992
A: Title: High-efficiency expression/cloning of epidermal growth factor-receptor-bind
A: Reference number: A46243; MUID: 93028373
A: Accession: A46243
A: Status: preliminary; not compared with conceptual translation
A: Molecule type: nucleic acid
A: Residues: 1-239 <WAR>
A: Note: sequence extracted from NCBI backbone (NCBIPI:115326)
C: Superfamily: crk transforming protein; SH2 homology; SH3 homology
C: Keywords: growth factor receptor
F: 44-149/Domain: SH2 homology <SH2>
F: 170-218/Domain: SH3 homology <SH3>

Query Match 63.7%; Score 1078; DB 2; Length 239;
Best Local Similarity 99.5%; Pred. No. 1.8e-73;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64
DB 33 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 92

QY 65 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALLEFYKHYLDTTTLIEPVARS 124
DB 93 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALLEFYKHYLDTTTLIEPVARS 152

QY 125 RQSGVILRQEAAYRVALFDNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 184
DB 153 RQSGVILRQEAAYRVALFDNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 212

QY 185 IPVYVEKYRPPASVSALIGNQSGS 211
DB 213 IPVYVEKYRPPASVSALIGNQSGS 239

RESULT 5
B45022 CRK-I - human

C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C:Accession: B45022
R:Matsumura, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A:Title: Two species of human CRK cDNA encode proteins with distinct biological activities
A:Reference number: A45022; MUID:92334347
A:Accession: B45022
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-204 <MAT>
A:Experimental source: embryonic lung cells
A>Note: sequence extracted from NCBI backbone (NCBIN:108771, NCBI:108772)
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:13-118/Domain: SH2 homology <SH2>
F:139-187/Domain: SH3 homology <SH3>

Query Match 62.1%; Score 1052; DB 2; Length 204;
Best Local Similarity 99.0%; Pred. No. 1.3e-71;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 64
DB 2 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 61

QY 65 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHYLDTTTLIEPVARS 124
DB 62 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHYLDTTTLIEPVARS 121

QY 125 RQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAEDSEGKRG 184
DB 122 RQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAEDSEGKRG 181

QY 185 IPVPVVEKYRPAASVSALIGG 206
DB 182 IPVPVVEKYRPAASVSALIGG 203

RESULT 6
S41754
CRKL protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S41754
R:ten Hoeve, J.; Morris, C.; Heisterkamp, N.; Groffen, J.
Oncogene 8, 2469-2474, 1993
A:Title: Isolation and chromosomal localization of CRKL, a human crk-like gene.
A:Reference number: S41754; MUID:93368949
A:Accession: S41754
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <TEN>
A:Cross-references: EMBL:X59656; NID:q416519; PIDN:CAA42199.1; PID:q416520
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:14-102/Domain: SH2 homology <SH2>
F:130-178/Domain: SH3 homology <SH3>

Query Match 54.2%; Score 917.5; DB 2; Length 303;
Best Local Similarity 56.6%; Pred. No. 2.4e-61;
Matches 185; Conservative 33; Mismatches 56; Indels 53; Gaps 6;

QY 5 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 64
DB 3 SARFDSRSRAWYMGVPSRQEAQTRLOQRHGMFLVRDSTSPGDYVLSVSENSRVSHYI 62

QY 65 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHYLDTTTLIEPVAR- 123
DB 63 INSLPNR-----RFGKIQDQEFHLPALLEFYKIHYLDTTTLIEPAPRY 105

QY 124 -----SRQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAED 177
DB 106 PSPPVGSVSAPNLPATAEENLEYVRLTYDFPCNDAAEDLPFKKGLLVIEKPEQWMSART 165

QY 178 SEGKRGMPVYVVEKYRPAASVSALIGGQEGSH-----PQLGPGPEP-PYAPQSVNTP 232
DB 166 KGRVGMIPVYVEK-----LVRSSPHKKGHNNSNSYGIPEPAHAYAQPTTTP 215

QY 233 LPNL-----QNGPIYARVIOKRVNAYDKTALALEVGLVKVTKINVSQGW 278
DB 216 LPTVASTPAAAINPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGLVIVKVTNRNINQGW 275

QY 279 EGECKRGHGFPTHVRLLDQONPDED 305
DB 276 EGEVNGRKGFLPFTHVKIFDPQNPDDN 302

RESULT 8
A44988
Transforming protein (gag-crk) - avian sarcoma virus (fragments)
C:Species: avian sarcoma virus
C:Date: 28-Apr-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C:Accession: A44988
R:Tsueh, H.; Chang, C.H.W.; Yoshida, M.; Vogt, P.K.
Oncogene 4, 1281-1284, 1989
A:Title: A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene.

Db 106 PSPPMGVSAPNLPATAEENLEYVRLTYDFPCNDAAEDLPFKKGLLVIEKPEQWMSARN 165
QY 178 SEGKRGMPVYVVEKYRPAASVSALIGGQEGSH-----PQLGPGPEP-PYAPQSVN-- 230
Db 166 KGRVGMIPVYVEK-----LVRSSPHKKGHNNSNSYGIPEPAHAYAQPTTTP 215
QY 231 -----TDLPLNLQNGPIYARVIOKRVNAYDKTALALEVGLVKVTKINVSQGW 278
Db 216 LPAVSGSPGAALPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGLVIVKVTNRNINQGW 275
QY 279 EGECKRGHGFPTHVRLLDQONPDED 305
Db 276 EGEVNGRKGFLPFTHVKIFDPQNPDDN 302

RESULT 7
S58352
SH2/SH3 adaptor protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
C:Accession: S58352
R:de Jong, R.; Haataja, L.; Voncken, J.W.; Heisterkamp, N.; Groffen, J.
submitted to the EMBL Data Library, August 1995
A:Description: Tyrosine phosphorylation of murine Crkl.
A:Reference number: S58352
A:Accession: S58352
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-303 <DEJ>
A:Cross-references: EMBL:X90648; NID:g945008; PIDN:CAA62220.1; PID:g945009
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:14-102/Domain: SH2 homology <SH2>
F:130-178/Domain: SH3 homology <SH3>

Query Match 53.8%; Score 911.5; DB 2; Length 303;
Best Local Similarity 56.0%; Pred. No. 6.6e-61;
Matches 183; Conservative 34; Mismatches 57; Indels 53; Gaps 6;

QY 5 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 64
DB 3 SARFDSRSRAWYMGVPSRQEAQTRLOQRHGMFLVRDSTSPGDYVLSVSENSRVSHYI 62

QY 65 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHYLDTTTLIEPVAR- 123
DB 63 INSLPNR-----RFGKIQDQEFHLPALLEFYKIHYLDTTTLIEPAPRY 105

QY 124 -----SRQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAED 177
DB 106 PSPPVGSVSAPNLPATAEENLEYVRLTYDFPCNDAAEDLPFKKGLLVIEKPEQWMSART 165

QY 178 SEGKRGMPVYVVEKYRPAASVSALIGGQEGSH-----PQLGPGPEP-PYAPQSVNTP 232
DB 166 KGRVGMIPVYVEK-----LVRSSPHKKGHNNSNSYGIPEPAHAYAQPTTTP 215

QY 233 LPNL-----QNGPIYARVIOKRVNAYDKTALALEVGLVKVTKINVSQGW 278
DB 216 LPTVASTPAAAINPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGLVIVKVTNRNINQGW 275

QY 279 EGECKRGHGFPTHVRLLDQONPDED 305
DB 276 EGEVNGRKGFLPFTHVKIFDPQNPDDN 302

RESULT 8
A44988
Transforming protein (gag-crk) - avian sarcoma virus (fragments)
C:Species: avian sarcoma virus
C:Date: 28-Apr-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C:Accession: A44988
R:Tsueh, H.; Chang, C.H.W.; Yoshida, M.; Vogt, P.K.
Oncogene 4, 1281-1284, 1989
A:Title: A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene.

A:Molecule type: mRNA
A:Residues: 1-217 <MAT>
A:Cross-references: EMBL:X62853; NID:g55762; PIDN:CAA44665.1; PID:g55763
R:Watanabe, K.; Fukuchi, T.; Hosoya, H.; Shirasawa, T.; Matuoka, K.; Miki, H.; Takenawa, J. Biol. Chem. 270, 13733-13739, 1995
A:Title: Splicing isoforms of rat Ash/Grb2. Isolation and characterization of the cDNA and characterization of the protein
A:Reference number: 155429; MUID:95293967
A:Accession: 155429
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-156,171-217 <RES>
A:Cross-references: GB:D49846; NID:g914956; PIDN:BAA08645.1; PID:g914957
A:Accession: 170120
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-59 <RE2>
A:Cross-references: GB:D49847; NID:g914960; PIDN:BAA08646.1; PID:g914961
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
C:Keywords: growth factor receptor
F:5-53/Domain: SH3 homology <SH31>
F:60-150/Domain: SH2 homology <SH2>
F:163-210/Domain: SH3 homology <SH32>

Query Match 13.2%; Score 224; DB 2; Length 217;
Best Local Similarity 27.9%; Pred. No. 1e-09;
Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSWYGRLSRQEAVALLOGQRH-GVFLVRDSTSPGDYVLSVSENSRVSHYII 65
Db 51 NYTEMKPHWFFGKIPRAKAEMLSKQRHDAFLIRESEAPGDFSLVKFGNDVQHFVK 110
QY 66 NSSGPRPPVPPSPAPQPPGVSRLRIGDQFDSLPALEFYKIHLYDTTTLIEPVARS 125
Db 111 LRDG-----AGKYFLWVVKFNSLNLVDYHR-----STS-----VSRNQ 144
QY 126 QGSGVILRQ-----BEAEYVRALFDNGNDEDLPFKKGDIILRDKPQEWNAEDSEG 180
Db 145 Q-----IFLRDIEQVQPTTYQALFDFPDQEDGELGFRGRGDFIHVMDNSDPNWKGA-CHG 200
QY 181 KRGMIPVPVY 190
Db 201 QTGMFPRNV 210

RESULT 12
A54688
Modular adaptor Grb2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jan-2000
C:Accession: A54688
R:Suen, K.L.; Bustelo, X.R.; Pawson, T.; Barbacid, M.
Mol. Cell. Biol. 13, 5500-5512, 1993
A:Title: Molecular cloning of the mouse grb2 gene: differential interaction of the Grb2
A:Reference number: A54688; MUID:93360985
A:Accession: A54688
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SUE>
A:Cross-references: GB:U07617; NID:g464004; PIDN:AAB40022.1; PID:g464005
C:Genetics:
A:Gene: grb2
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:5-53/Domain: SH3 homology <SH31>
F:60-150/Domain: SH2 homology <SH2>
F:163-210/Domain: SH3 homology <SH32>

Query Match 13.2%; Score 224; DB 2; Length 217;
Best Local Similarity 27.9%; Pred. No. 1e-09;
Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSWYGRLSRQEAVALLOGQRH-GVFLVRDSTSPGDYVLSVSENSRVSHYII 65
Db 51 NYTEMKPHWFFGKIPRAKAEMLSKQRHDAFLIRESEAPGDFSLVKFGNDVQHFVK 110
QY 66 NSSGPRPPVPPSPAPQPPGVSRLRIGDQFDSLPALEFYKIHLYDTTTLIEPVARS 125
Db 111 LRDG-----AGKYFLWVVKFNSLNLVDYHR-----STS-----VSRNQ 144
QY 126 QGSGVILRQ-----BEAEYVRALFDNGNDEDLPFKKGDIILRDKPQEWNAEDSEG 180
Db 145 Q-----IFLRDIEQVQPTTYQALFDFPDQEDGELGFRGRGDFIHVMDNSDPNWKGA-CHG 200
QY 181 KRGMIPVPVY 190
Db 201 QTGMFPRNV 210

RESULT 12
A54688
Modular adaptor Grb2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jan-2000
C:Accession: A54688
R:Suen, K.L.; Bustelo, X.R.; Pawson, T.; Barbacid, M.
Mol. Cell. Biol. 13, 5500-5512, 1993
A:Title: Molecular cloning of the mouse grb2 gene: differential interaction of the Grb2
A:Reference number: A54688; MUID:93360985
A:Accession: A54688
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SUE>
A:Cross-references: GB:U07617; NID:g464004; PIDN:AAB40022.1; PID:g464005
C:Genetics:
A:Gene: grb2
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:5-53/Domain: SH3 homology <SH31>
F:60-150/Domain: SH2 homology <SH2>
F:163-210/Domain: SH3 homology <SH32>

Db 51 NYTEMKPHWFFGKIPRAKAEMLSKQRHDAFLIRESEAPGDFSLVKFGNDVQHFVK 110
QY 66 NSSGPRPPVPPSPAPQPPGVSRLRIGDQFDSLPALEFYKIHLYDTTTLIEPVARS 125
Db 111 LRDG-----AGKYFLWVVKFNSLNLVDYHR-----STS-----VSRNQ 144
QY 126 QGSGVILRQ-----BEAEYVRALFDNGNDEDLPFKKGDIILRDKPQEWNAEDSEG 180
Db 145 Q-----IFLRDIEQVQPTTYQALFDFPDQEDGELGFRGRGDFIHVMDNSDPNWKGA-CHG 200
QY 181 KRGMIPVPVY 190
Db 201 QTGMFPRNV 210

RESULT 13
A43321
growth factor receptor-bound protein 2 - human
N:Alternate names: abundant-src-homology (ash) protein
N:Contains: growth factor receptor-bound protein 3-3
C:Species: Homo sapiens (man)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A43321; A54064; A46278
R:Lowenstein, E.J.; Dally, R.J.; Batzer, A.G.; Li, W.; Margolis, B.; Lammers, R.; Ullr
Cell 70, 431-442, 1992
A:Title: The SH2 and SH3 domain-containing protein GRB2 links receptor tyrosine kinases
A:Reference number: A43321; MUID:92354060
A:Accession: A43321
A:Molecule type: mRNA
A:Residues: 1-217 <LOW>
A:Cross-references: GB:M96995; NID:g181975; PIDN:AAA58448.1; PID:g181976
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIN:110294, NCBI:P110295)
R:Rath, I.; Schweighoffer, F.; Rey, I.; Multon, M.C.; Boiziau, J.; Duchesne, M.; Tocq
Science 264, 971-974, 1994
A:Title: Cloning of a Grb2 isoform with apoptotic properties.
A:Reference number: A54064; MUID:94233382
A:Accession: A54064
A:Molecule type: mRNA
A:Residues: 1-59, 101-217 <PAT>
A:Cross-references: GB:L29511; NID:g460667; PIDN:AAC37549.1; PID:g498178
R:Matuoka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992
A:Title: Cloning of ASH, a ubiquitous protein composed of one Src homology region (SH
A:Reference number: S26050; MUID:93028395
A:Accession: A46278
A:Molecule type: mRNA
A:Residues: 58-217 <MAT>
A:Cross-references: EMBL:X62852; NID:g28875; PIDN:CAA44664.1; PID:g28876
C:Genetics:
A:Gene: GDB:GRB2
A:Cross-references: GDB:134732; OMIM:600180
A:Map position: 17q24-17q25
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
C:Keywords: alternative splicing; growth factor receptor
F:1-217/Product: growth factor receptor-bound protein 2 #status predicted <LSF>
F:1-59,101-217/Product: growth factor receptor-bound protein 3-3 #status predicted <S>
F:5-53/Domain: SH3 homology <SH31>
F:60-150/Domain: SH2 homology <SH2>
F:163-210/Domain: SH3 homology <SH32>

Query Match 13.2%; Score 224; DB 2; Length 217;
Best Local Similarity 27.9%; Pred. No. 1e-09;
Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSWYGRLSRQEAVALLOGQRH-GVFLVRDSTSPGDYVLSVSENSRVSHYII 65
Db 51 NYTEMKPHWFFGKIPRAKAEMLSKQRHDAFLIRESEAPGDFSLVKFGNDVQHFVK 110
QY 66 NSSGPRPPVPPSPAPQPPGVSRLRIGDQFDSLPALEFYKIHLYDTTTLIEPVARS 125
Db 111 LRDG-----AGKYFLWVVKFNSLNLVDYHR-----STS-----VSRNQ 144
QY 126 QGSGVILRQ-----BEAEYVRALFDNGNDEDLPFKKGDIILRDKPQEWNAEDSEG 180
Db 145 Q-----IFLRDIEQVQPTTYQALFDFPDQEDGELGFRGRGDFIHVMDNSDPNWKGA-CHG 200
QY 181 KRGMIPVPVY 190
Db 201 QTGMFPRNV 210

RESULT 13
A43321
growth factor receptor-bound protein 2 - human
N:Alternate names: abundant-src-homology (ash) protein
N:Contains: growth factor receptor-bound protein 3-3
C:Species: Homo sapiens (man)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A43321; A54064; A46278
R:Lowenstein, E.J.; Dally, R.J.; Batzer, A.G.; Li, W.; Margolis, B.; Lammers, R.; Ullr
Cell 70, 431-442, 1992
A:Title: The SH2 and SH3 domain-containing protein GRB2 links receptor tyrosine kinases
A:Reference number: A43321; MUID:92354060
A:Accession: A43321
A:Molecule type: mRNA
A:Residues: 1-217 <LOW>
A:Cross-references: GB:M96995; NID:g181975; PIDN:AAA58448.1; PID:g181976
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIN:110294, NCBI:P110295)
R:Rath, I.; Schweighoffer, F.; Rey, I.; Multon, M.C.; Boiziau, J.; Duchesne, M.; Tocq
Science 264, 971-974, 1994
A:Title: Cloning of a Grb2 isoform with apoptotic properties.
A:Reference number: A54064; MUID:94233382
A:Accession: A54064
A:Molecule type: mRNA
A:Residues: 1-59, 101-217 <PAT>
A:Cross-references: GB:L29511; NID:g460667; PIDN:AAC37549.1; PID:g498178
R:Matuoka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992
A:Title: Cloning of ASH, a ubiquitous protein composed of one Src homology region (SH
A:Reference number: S26050; MUID:93028395
A:Accession: A46278
A:Molecule type: mRNA
A:Residues: 58-217 <MAT>
A:Cross-references: EMBL:X62852; NID:g28875; PIDN:CAA44664.1; PID:g28876
C:Genetics:
A:Gene: GDB:GRB2
A:Cross-references: GDB:134732; OMIM:600180
A:Map position: 17q24-17q25
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
C:Keywords: alternative splicing; growth factor receptor
F:1-217/Product: growth factor receptor-bound protein 2 #status predicted <LSF>
F:1-59,101-217/Product: growth factor receptor-bound protein 3-3 #status predicted <S>
F:5-53/Domain: SH3 homology <SH31>
F:60-150/Domain: SH2 homology <SH2>
F:163-210/Domain: SH3 homology <SH32>

Db 111 LRDC-----AGKFLWVVKFNSLNELVDYHR-----STS-----VSRNQ 144

QY 126 QGSGVILRQ-----EEAEYVRALFDNGNDEEDLPKKGDIILIRDKPPEQWNAEDSEG 180

Db 145 Q---IFLRDIEQVPQPTTYVQALFDQEDGELGFRRGDFIHVMDSNDFNWKGA-CHG 200

QY 181 KRGMIPVPYV 190

Db 201 QTGMFPRNYV 210

RESULT 14

JT0664

growth factor receptor-binding protein GRB2 homolog - chicken

C:Species: Gallus gallus (chicken)

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jan-2000

C:Accession: JT0664

R:Wasenius, V.M.; Merilaelinen, J.; Lehto, V.P.

Gene 134, 299-300, 1993

A:Title: Sequence of a chicken cDNA encoding a GRB2 protein.

A:Reference number: JT0664; MUID:94085795

A:Accession: JT0664

A:Molecule type: mRNA

A:Residues: 1-217 <WAS>

A:Cross-references: GB:I19258; NID:G304385; PIDN:AAAI6318.1; PID:G304386

C:Comment: GRB2 protein plays a role in mediating the critical linkage between growth factor receptor and Ras.

C:Superfamily: crk transforming protein; SH2 homology; SH3 homology

C:Keywords: growth factor receptor

F:5-53/Domain: SH3 homology <SH3>

F:60-150/Domain: SH2 homology <SH2>

F:163-210/Domain: SH3 homology <SH32>

Query Match 12.9%; Score 218; DB 2; Length 217;

Best Local Similarity 27.9%; Pred. No. 2.8e-09;

Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSWYWGRLSRQEAVALLOGRH-GVFLVRDSTSPGDIYVLSVSENSRVSHYII 65

Db 51 NYIEMKPHWFFGKIPRAKAEMLGQRHDGAPLIRESSEAFCDLSLVKFGNDVQOFKV 110

QY 66 NSSGPRPPVPPSPAQPPGVSPRLRIGDQEDSLPALLEFYKIHVLDTTTLEIPIVARSR 125

Db 111 LRDC-----AGKYLWVVKFNSLNELVDYHR-----STS-----VSRNQ 144

QY 126 QGSGVILRQ-----EEAEYVRALFDNGNDEEDLPKKGDIILIRDKPPEQWNAEDSEG 180

Db 145 Q---IFLRDIEQVPQPTTYVQALFDQEDGELGFRRGDFIQVLDNSDFNWKGA-CHG 200

QY 181 KRGMIPVPYV 190

Db 201 QTGMFPRNYV 210

RESULT 15

S25730

SH2-SH3 protein sem-5 - Caenorhabditis elegans

N:Alternate names: sex-muscle-abnormal protein 5 (sem-5)

C:Species: Caenorhabditis elegans

C:Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000

C:Accession: S25730; T15499

R:Clark, S.G.; Stern, M.J.; Horvitz, H.R.

Nature 356, 340-344, 1992

A:Title: C. elegans cell-signalling gene sem-5 encodes a protein with SH2 and SH3 domain

A:Reference number: S25730; MUID:92195405

A:Accession: S25730

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-228 <CIA>

A:Cross-references: GB:S88446; NID:Q247604; PID:Q247605

R:Minx, P.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid C14F5.

A:Reference number: Z18361

A:Accession: T15499

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-228 <MIN>

A:Cross-references: EMBL:U29082; NID:9861384; PID:9861389; PIDN:AAA68405.1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: sem-5

A:Introns: 26/3; 60/2; 101/2; 137/2; 183/1

C:Superfamily: crk transforming protein; SH2 homology; SH3 homology

F:5-53/Domain: SH3 homology <SH31>

F:60-151/Domain: SH2 homology <SH2>

F:161-208/Domain: SH3 homology <SH32>

Query Match 11.9%; Score 202; DB 2; Length 228;

Best Local Similarity 25.1%; Pred. No. 4.7e-08;

Matches 54; Conservative 39; Mismatches 68; Indels 54; Gaps 6;

QY 7 NFDSEERSWYWGRLSRQEAVALLOGQ--RHGVFLVRDSTSPGDIYVLSVSENSRVSHYI 64

Db 51 NYIRWTECNWYLGKITRNDAEVLLKPTVRDGHFLVRQCESSPGFEFSISVRFQDSVQHF 110

QY 65 INSSGPRPPVPPSPAQPPGVSPSRLRIGDQ-----EFDSPALLEFYKIHVLDTT 115

Db 111 V-----LTDQNGKYLLWVVKFNSLNELVAYHRTASVSR 144

QY 116 TLIEPIVARSGSGVILRQE---EAEYVRALFDNGNDEEDLPKKGDIILIRDKPPEQW 172

Db 145 -----HTLLSDMNVEVKFVQALFDENFQESGELAFKRGDVTILNKDDPNW 191

QY 173 WNAEDSEKRGKMIPIVYVEKYRPAASVSALIGN 207

Db 192 WEGQ-LNNRRGIFPSNYVCPYNSKNKSNVAPGFN 225

Search completed: September 27, 2001, 16:42:23

Job time: 191 sec
